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RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/513,365A

TIME: 08:37:38

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ENTERED

3 <110> APPLICANT: Harris, Curtis C
 4 Nagashima, Makoto
 5 Government of United States as represented by the Secretary of the
 6 Department of Health and Human Services
 8 <120> TITLE OF INVENTION: New Tumor Suppressor Gene P33ING2
 10 <130> FILE REFERENCE: 015280-376100US
 12 <140> CURRENT APPLICATION NUMBER: US 09/513,365A
 13 <141> CURRENT FILING DATE: 2000-02-25
 15 <150> PRIOR APPLICATION NUMBER: US 60/121,891
 16 <151> PRIOR FILING DATE: 1999-02-26
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 280
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: p33ING2
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 33 1 5 10 15
 35 Thr Gly Glu Arg Ser Arg Leu Leu Thr Cys Tyr Val Gln Asp Tyr Leu
 36 20 25 30
 38 Glu Cys Val Glu Ser Leu Pro His Asp Met Gln Arg Asn Val Ser Val
 39 35 40 45
 41 Leu Arg Glu Leu Asp Asn Lys Tyr Gln Glu Thr Leu Lys Glu Ile Asp
 42 50 55 60
 44 Asp Val Tyr Glu Lys Tyr Lys Lys Glu Asp Asp Leu Asn Gln Lys Lys
 45 65 70 75 80
 47 Arg Leu Gln Gln Leu Leu Gln Arg Ala Leu Ile Asn Ser Gln Glu Leu
 48 85 90 95
 50 Gly Asp Glu Lys Ile Gln Ile Val Thr Gln Met Leu Glu Leu Val Glu
 51 100 105 110
 53 Asn Arg Ala Arg Gln Met Glu Leu His Ser Gln Cys Phe Gln Asp Pro
 54 115 120 125
 56 Ala Glu Ser Glu Arg Ala Ser Asp Lys Ala Lys Met Asp Ser Ser Gln
 57 130 135 140
 59 Pro Glu Arg Ser Ser Arg Arg Pro Arg Arg Gln Arg Thr Ser Glu Ser
 60 145 150 155 160
 62 Arg Asp Leu Cys His Met Ala Asn Gly Ile Glu Asp Cys Asp Asp Gln
 63 165 170 175
 65 Pro Pro Lys Glu Lys Lys Ser Lys Ser Ala Lys Lys Lys Lys Arg Ser
 66 180 185 190
 68 Lys Ala Lys Gln Glu Arg Glu Ala Ser Pro Val Glu Phe Ala Ile Asp
 69 195 200 205
 71 Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu

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72      210      215      220
74 Met Ile Gly Cys Asp Asn Gln Cys Pro Ile Glu Trp Phe His Phe
75 225      230      235      240
77 Ser Cys Val Ser Leu Thr Tyr Lys Pro Lys Gly Lys Trp Tyr Cys Pro
78      245      250      255
80 Lys Cys Arg Gly Asp Asn Glu Lys Thr Met Asp Lys Ser Thr Glu Lys
81      260      265      270
83 Thr Lys Lys Asp Arg Arg Ser Arg
84      275      280
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88 <211> LENGTH: 1080
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Description of Artificial Sequence: p33ING2
94     nucleic acid sequence (GenBank Accession No.
95     AF05053537)
97 <400> SEQUENCE: 2
98 gcggccgcgg ccggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcgga 60
99 cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg 120
100 ggagcggagc cggctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt 180
101 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaaga 240
102 aacgttaaag gaaattgatg atgtctacga aaaatataag aaagaagatg atttaaacca 300
103 gaagaaacgt ctacagcagc ttctccagag agcactaatt aatagtcaag aattgggaga 360
104 tgaaaaaata cagattgtta cacaaatgct cgaattggtg gaaaatcggg caagacaaat 420
105 ggagttacac tcacagtgtt tccaagatcc tgctgaaagt gaacgagcct cagataaagc 480
106 aaagatggat tccagccaac cagaaagatc ttcaagaaga ccccgaggc agcggaccag 540
107 tgaaagccgt gatttatgtc acatggcaaa tgggattgaa gactgtgatg atcagccacc 600
108 taaagaaaag aaatccaagt cagcaaagaa aaagaaacgc tccaaggcca agcaggaaag 660
109 ggaagcttca cctgttgagt ttgcaataga tcctaataa cctacatact gcttatgcaa 720
110 ccaagtgtct tatggggaga tgataggatg tgacaatgaa cagtgtccaa ttgaatggtt 780
111 tcaacttttca tgtgtttcac ttacctataa accaaagggg aaatggtatt gccc aaagtg 840
112 caggggagat aatgagaaaa caatggacaa aagtactgaa aagacaaaaa aggatagaag 900
113 atcgaggtag taaaggccat ccacatttta aagggttatt tgtcttttat ataattcggt 960
114 tgcttttcaga aaatgtttta gggtaaatgc ataagactat gcaataattt ttaatcatta 1020
115 gtattaatgg tgtattaaaa gttgtgttac tttgaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
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119 <211> LENGTH: 7
120 <212> TYPE: PRT
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123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerate
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127 <400> SEQUENCE: 3
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129 1      5
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 7
134 <212> TYPE: PRT

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135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerate
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141 <400> SEQUENCE: 4
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147 <211> LENGTH: 20
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide 7-26
153     of p33ING2 (KMP1)
155 <400> SEQUENCE: 5
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159 Leu Leu Thr Cys
160           20
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164 <211> LENGTH: 280
165 <212> TYPE: PRT
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168 <220> FEATURE:
169 <223> OTHER INFORMATION: Description of Artificial Sequence: missense
170     p33ING2 sequence - Arg 153 to Ser
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176 Thr Gly Glu Arg Ser Arg Leu Leu Thr Cys Tyr Val Gln Asp Tyr Leu
177           20           25           30
179 Glu Cys Val Glu Ser Leu Pro His Asp Met Gln Arg Asn Val Ser Val
180           35           40           45
182 Leu Arg Glu Leu Asp Asn Lys Tyr Gln Glu Thr Leu Lys Glu Ile Asp
183           50           55           60
185 Asp Val Tyr Glu Lys Tyr Lys Lys Glu Asp Asp Leu Asn Gln Lys Lys
186   65           70           75           80
188 Arg Leu Gln Gln Leu Leu Gln Arg Ala Leu Ile Asn Ser Gln Glu Leu
189           85           90           95
191 Gly Asp Glu Lys Ile Gln Ile Val Thr Gln Met Leu Glu Leu Val Glu
192           100          105          110
194 Asn Arg Ala Arg Gln Met Glu Leu His Ser Gln Cys Phe Gln Asp Pro
195           115          120          125
197 Ala Glu Ser Glu Arg Ala Ser Asp Lys Ala Lys Met Asp Ser Ser Gln
198           130          135          140
200 Pro Glu Arg Ser Ser Arg Arg Pro Ser Arg Gln Arg Thr Ser Glu Ser
201   145          150          155          160
203 Arg Asp Leu Cys His Met Ala Asn Gly Ile Glu Asp Cys Asp Asp Gln
204           165          170          175

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206 Pro Pro Lys Glu Lys Lys Ser Lys Ser Ala Lys Lys Lys Lys Arg Ser
207          180          185          190
209 Lys Ala Lys Gln Glu Arg Glu Ala Ser Pro Val Glu Phe Ala Ile Asp
210          195          200          205
212 Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu
213          210          215          220
215 Met Ile Gly Cys Asp Asn Glu Gln Cys Pro Ile Glu Trp Phe His Phe
216 225          230          235          240
218 Ser Cys Val Ser Leu Thr Tyr Lys Pro Lys Gly Lys Trp Tyr Cys Pro
219          245          250          255
221 Lys Cys Arg Gly Asp Asn Glu Lys Thr Met Asp Lys Ser Thr Glu Lys
222          260          265          270
224 Thr Lys Lys Asp Arg Arg Ser Arg
225          275          280
228 <210> SEQ ID NO: 7
229 <211> LENGTH: 423
230 <212> TYPE: DNA
231 <213> ORGANISM: Homo sapiens
233 <220> FEATURE:
234 <223> OTHER INFORMATION: p 33ING2 genomic DNA sequence (exon 1/intron)
235 GenBank Accession No. HSING2S1
237 <221> NAME/KEY: exon
238 <222> LOCATION: (1)..(239)
240 <221> NAME/KEY: intron
241 <222> LOCATION: (240)..(>423)
243 <400> SEQUENCE: 7
244 gcgggcgcgcg cgggtgcatg tgcggctgct ggatgcggag gcggcggcga cggcgcggat 60
245 cggcaggatg ttagggcagc agcagcagca actgtactcg tcggctgcgc tcctgaccgg 120
246 ggagcgggagc cggtctgctca cctgctacgt gcaggactac cttgagtgcg tggagtgcgt 180
247 gccccacgac atgcagagga acgtgtctgt gctgcgagag ctggacaaca aatatcaagg 240
248 taggggcccgc ggggctgccg gcctcgggag ccggtggcgg ggagcctgtc cgggggagtg 300
249 ccaccttccc tttctcccg tgcagtcctc ccgagcgcac cgagggctctg ccgagcggga 360
250 ctgggaggac tggagaccgg gttggcggcc ctccgtggcc ccgcggtggg cgagtgaagg 420
251 aga 423
254 <210> SEQ ID NO: 8
255 <211> LENGTH: 279
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: p33ING1
262 <400> SEQUENCE: 8
263 Met Leu Ser Pro Ala Asn Gly Glu Gln Leu His Leu Val Asn Tyr Val
264 1 5 10 15
266 Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
267 20 25 30
269 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
270 35 40 45
272 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
273 50 55 60

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275 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
276 65 70 75 80
278 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
279 85 90 95
281 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
282 100 105 110
284 Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Ala Gly Asn Ser Gly Lys
285 115 120 125
287 Ala Gly Ala Asp Arg Pro Lys Gly Glu Ala Ala Ala Gln Ala Asp Lys
288 130 135 140
290 Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
291 145 150 155 160
293 Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
294 165 170 175
296 Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Arg Ser Lys Ala
297 180 185 190
299 Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
300 195 200 205
302 Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
303 210 215 220
305 Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
306 225 230 235 240
308 Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
309 245 250 255
311 Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
312 260 265 270
314 Lys Glu Arg Ala Tyr Asn Arg
315 275
318 <210> SEQ ID NO: 9
319 <211> LENGTH: 279
320 <212> TYPE: PRT
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide 1-17
325 and C of p33ING1 (KMP2)
327 <400> SEQUENCE: 9
328 Met Leu Ser Pro Ala Asn Gly Glu Gln Leu His Leu Val Asn Tyr Val
329 1 5 10 15
331 Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
332 20 25 30
334 Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
335 35 40 45
337 Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
338 50 55 60
340 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
341 65 70 75 80
343 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
344 85 90 95
346 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/513,365A

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